

RAW SEQUENCE LISTING

DATE: 04/22/2001

PATENT APPLICATION: US/09/463,480

TIME: 14:21:24

Input Set : A:\13334.asc

Output Set: N:\CRF3\04222001\I463480.raw

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4 <110> APPLICANT: Singh, Mohan
5      Bhalla, Prem
6      Hui-Ling, Xu
7      Swoboda, Ines
9 <120> TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES THEREFOR
11 <130> FILE REFERENCE: 13334
13 <140> CURRENT APPLICATION NUMBER: 09/463,480
14 <141> CURRENT FILING DATE: 2000-04-07
16 <160> NUMBER OF SEQ ID NOS: 11
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 24
22 <212> TYPE: DNA
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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36 <213> ORGANISM: Artificial Sequence
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39 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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49 <213> ORGANISM: Lilium longiflorum
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52 <221> NAME/KEY: CDS
53 <222> LOCATION: (82)..(468)
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58 ggggtactctt aagcatataaa c atg agg gcg gtg gcg gtt ttc ttt gct tgc 111
59                      Met Arg Ala Val Ala Val Phe Phe Ala Cys
60                      1                      5                      10
62 gtt ctc ttc tgt atg gtt cac aaa gcc gca ctt gcg gat gat aaa acg 159
63 Val Leu Phe Cys Met Val His Lys Ala Ala Leu Ala Asp Asp Lys Thr
64                      15                      20                      25
66 tgc aac cct aca gat ttt atg gtt acc caa acc ata act gga ttg aca 207
67 Cys Asn Pro Thr Asp Phe Met Val Thr Gln Thr Ile Thr Gly Leu Thr
68                      30                      35                      40
70 atc ggc ggt aaa caa gag ttc gag gtc aat tta ata aac aat ttg tat 255
71 Ile Gly Gly Lys Gln Glu Phe Glu Val Asn Leu Ile Asn Asn Leu Tyr
72                      45                      50                      55

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74 tgt gca caa tct aat gtc aaa gtt tca tgt gac ggg ctt cat acc acc 303
75 Cys Ala Gln Ser Asn Val Lys Val Ser Cys Asp Gly Leu His Thr Thr
76      60      65      70
78 gaa cca ata gat cct cac att atc aga cca ctt agt gac gga acg aac 351
79 Glu Pro Ile Asp Pro His Ile Ile Arg Pro Leu Ser Asp Gly Thr Asn
80 75      80      85      90
82 aac tgc ctt gtc aac aat gga gcg cct att tct cat gct act ctt gta 399
83 Asn Cys Leu Val Asn Asn Gly Ala Pro Ile Ser His Ala Thr Leu Val
84      95      100      105
86 gca ttc aag tat gcc tgg gat gtt cct cca tct ttc agc atc atc agc 447
87 Ala Phe Lys Tyr Ala Trp Asp Val Pro Pro Ser Phe Ser Ile Ile Ser
88      110      115      120
90 tct gat ata aat tgc tcc taa ggagaaaatt ctagttggca gagaataatc 498
91 Ser Asp Ile Asn Cys Ser
92      125
94 atatagtctt ttttactgag ctatttaatt ttttcaattt toaccaataa gattatttta 558
96 atggaatggt aatgtattag aattgaaaaa taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 618
98 aaaaaaa 625
102 <210> SEQ ID NO 4
103 <211> LENGTH: 128
104 <212> TYPE: PRT
105 <213> ORGANISM: Lilium longiflorum
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108 Met Arg Ala Val Ala Val Phe Phe Ala Cys Val Leu Phe Cys Met Val
109 1 5 10 15
110 His Lys Ala Ala Leu Ala Asp Asp Lys Thr Cys Asn Pro Thr Asp Phe
111 20 25 30
112 Met Val Thr Gln Thr Ile Thr Gly Leu Thr Ile Gly Gly Lys Gln Glu
113 35 40 45
114 Phe Glu Val Asn Leu Ile Asn Asn Leu Tyr Cys Ala Gln Ser Asn Val
115 50 55 60
116 Lys Val Ser Cys Asp Gly Leu His Thr Thr Glu Pro Ile Asp Pro His
117 65 70 75 80
118 Ile Ile Arg Pro Leu Ser Asp Gly Thr Asn Asn Cys Leu Val Asn Asn
119 85 90 95
120 Gly Ala Pro Ile Ser His Ala Thr Leu Val Ala Phe Lys Tyr Ala Trp
121 100 105 110
122 Asp Val Pro Pro Ser Phe Ser Ile Ile Ser Ser Asp Ile Asn Cys Ser
123 115 120 125
126 <210> SEQ ID NO: 5
127 <211> LENGTH: 587
128 <212> TYPE: DNA
129 <213> ORGANISM: Lilium longiflorum
131 <220> FEATURE:
132 <221> NAME/KEY: CDS
133 <222> LOCATION: (49)..(378)
135 <400> SEQUENCE: 5
136 gaaagttgaa acatctccat caaactctag agtcagattt cccacaag atg att tca 57
137 Met Ile Ser

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138                                     1
140 tgc gca aat aac aaa ggc gcc ggc aca agc cgc cgc aag ctc cgt tct 105
141 Ser Ala Asn Asn Lys Gly Ala Gly Thr Ser Arg Arg Lys Leu Arg Ser
142      5              10              15
144 gag aag gct gca ctc cag ttc tcc gtc agt cgc gtc gaa tac tcc ctc 153
145 Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu Tyr Ser Leu
146 20      25              30              35
148 aag aag ggg cgc tat tgc agg cgc tta ggc gct acg gcc ccc gtc tac 201
149 Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala Pro Val Tyr
150      40              45              50
152 cta gcc gcc gtc ctt gaa aac ctc gtg gcc gaa gtg ttg gac atg gag 249
153 Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu Asp Met Ala
154      55              60              65
156 gag aac gtg aca gaa gaa aca tcc ccc att gtt atc aaa ccg agg cat 297
157 Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys Pro Arg His
158      70              75              80
160 att atg ctt gcc ccc agg aat gat gta gaa gtt gaa caa gct gtt tca 345
161 Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln Ala Val Ser
162      85              90              95
164 cgg tgt cac cat ctc ggc atc agg tgt cgt ccc taaaaacacgc aaagagctgg 398
165 Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
166 100              105              110
168 accgtcgcaa acgcggttcc acctttcagc cggattagtt cttgatattt cattctatca 458
170 atcttggtta tgtgactgtg atttttcggt ttgtgttgaa ctaagccccc taatctggat 518
173 ttctcggttt atgttgaact aagtctgtgc actcttgaag taaaaaaaaa aaaaaaaaaa 578
175 aaaaaaaaaa 587
179 <210> SEQ ID NO: 6
180 <211> LENGTH: 110
181 <212> TYPE: PRT
182 <213> ORGANISM: Lilium longiflorum
184 <400> SEQUENCE: 6
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186 1      5              10              15
188 Leu Arg Ser Glu Lys Ala Ala Leu Gln Phe Ser Val Ser Arg Val Glu
189      20              25              30
191 Tyr Ser Leu Lys Lys Gly Arg Tyr Cys Arg Arg Leu Gly Ala Thr Ala
192      35              40              45
194 Pro Val Tyr Leu Ala Ala Val Leu Glu Asn Leu Val Ala Glu Val Leu
195      50              55              60
197 Asp Met Ala Ala Asn Val Thr Glu Glu Thr Ser Pro Ile Val Ile Lys
198      65              70              75              80
200 Pro Arg His Ile Met Leu Ala Pro Arg Asn Asp Val Glu Val Glu Gln
201      85              90              95
203 Ala Val Ser Arg Cys His His Leu Gly Ile Arg Cys Arg Pro
204      100              105              110
209 <210> SEQ ID NO: 7
210 <211> LENGTH: 485
211 <212> TYPE: DNA
212 <213> ORGANISM: Lilium longiflorum

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214 <220> FEATURE:
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216 <222> LOCATION: (16)..(348)
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220           Met Thr Ile Pro Glu Lys Lys Ser Val Ala Pro Met
221           1           5           10
223 gcc cgt atg aag cat aca gcc cgc atg tct acc gcc ggt aag gct cca 99
224 Ala Arg Met Lys His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro
225           15           20           25
227 cgc aag cag ctc gcc tct aag gct ctt cgc aag gcg cca cca cca ccg 147
228 Arg Lys Gln Leu Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro
229           30           35           40
231 acc aaa gga gtg aag cag ccc acc act acc acc tcc gga aaa tgg cgc 195
232 Thr Lys Gly Val Lys Gln Pro Thr Thr Thr Ser Gly Lys Trp Arg
233           45           50           55           60
235 ttc acg aga ttt cac agg aaa ctg cca ttc caa ggg ctg gtg agg aaa 243
236 Phe Ala Arg Phe His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys
237           65           70           75
239 atc tgg cag gac ttg aag aca cat ctg cgc ttc aag aac cac tcg gtt 291
240 Ile Trp Gln Asp Leu Lys Thr His Leu Arg Phe Lys Asn His Ser Val
241           80           85           90
243 cct cca ctt gag gag gta act gag gtt tat cct tgc caa act att gga 339
244 Pro Pro Leu Glu Glu Val Thr Glu Val Tyr Pro Cys Gln Thr Ile Gly
245           95           100           105
247 gga tgc tat taggatattg aatttgata atggtttaat tatctgttct 388
248 Gly Cys Tyr
249           110
251 acctttatga tcaaatttct gtggctcagc gttgtgtaat ttgggcaatc gaattcttag 448
253 ctatatggcc tcaaaaaaaaa aaaaaaaaaa aaaaaaa 485
257 <210> SEQ ID NO: 8
258 <211> LENGTH: 111
259 <212> TYPE: PRT
260 <213> ORGANISM: Lilium longiflorum
262 <400> SEQUENCE: 8
263 Met Thr Ile Pro Glu Lys Lys Ser Val Ala Pro Met Ala Arg Met Lys
264   1           5           10           15
266 His Thr Ala Arg Met Ser Thr Gly Gly Lys Ala Pro Arg Lys Gln Leu
267           20           25           30
269 Ala Ser Lys Ala Leu Arg Lys Ala Pro Pro Pro Pro Thr Lys Gly Val
270           35           40           45
272 Lys Gln Pro Thr Thr Thr Thr Ser Gly Lys Trp Arg Phe Ala Arg Phe
273           50           55           60
275 His Arg Lys Leu Pro Phe Gln Gly Leu Val Arg Lys Ile Trp Gln Asp
276           65           70           75           80
279 Leu Lys Thr His Leu Arg Phe Lys Asn His Ser Val Pro Pro Leu Glu
280           85           90           95
282 Glu Val Thr Glu Val Tyr Pro Cys Gln Thr Ile Gly Gly Cys Tyr
283           100           105           110

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287 <210> SEQ ID NO: 9
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295 tgtctatttc tataggcatg atttagtagt gagttaatta tcctataatt tctcttcttg 120
297 tatgtcctaaa taactgggttc tttaatgaat agataattaa gttttgtagc aatttcttcc 180
299 tcaaatgtgag tatcaacaat tgttagattg ctttgggtgat tatatttgat ataattgttt 240
301 gtaagaatgt gtagtgaaaa gattgtgatt attcatttcg ttgttggacg aattgtttaga 300
303 gccccatcgc taatgcotta tagtactcga aatatgttgg gaatagaaga tgaaaaatcc 360
305 cattctttgt agtaggagta aaaatttgtc ttttcattat tccattgaat gtttaaccact 420
307 tgcattcatc ctgacgggga tggcagagtt ccgaccatct agtgatccgt gggatattga 480
309 ttttggtgtg tcaatgaaat tgtgagaacg ggcttctggg agagaaaagc cctcttgctt 540
311 ctgatatgaa cactgaggct gattatgtta acggatggag atttatcagt ggcgaattt 600
313 ggggtgctgta gagacagaat ttgaaagttc taacaataaa ccctaattct gaacttgggc 660
315 ggggctggga ttttactctt aacgtgaaga gaggcaagat gaattgacag cttggaagtc 720
317 aatccagtat ttgcagcagt cgtgacgaat tgggttgaca gttacatcgg tcagagaatg 780
319 cgttctataa attcccccaa tgcggcagtg aaaatcccat cccatcaaca gaagttttaa 840
321 gtggaaaccc attccaatag agaagatcga acaaagggtg tttaaacata caaatggggg 900
323 cagtggtgtt tctttttgct tgcgttctct tctgtatggt tcaca 945
327 <210> SEQ ID NO: 10
328 <211> LENGTH: 24
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial Sequence
332 <220> FEATURE:
333 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
335 <400> SEQUENCE: 10
336 caggcatact tgaatgctac aaga 24
340 <210> SEQ ID NO: 11
341 <211> LENGTH: 24
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
348 <400> SEQUENCE: 11
349 tgtgaaccat acagaagaga acgc 24

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VERIFICATION SUMMARY

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